

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:35:04 ; Search time 2798 Seconds

(without alignments)
9888.466 Million cell updates/sec

Title: US-10-627-141-14

Sequence: 1 TTCATACAGTAAAGCCGACCCAGC.....CTTACATCCCTGTAGTTCG 571

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hlg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pac: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sbs: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	6	AR432668 Sequence
2	567.8	99.4	571	6	AR432670 Sequence
3	566.2	99.2	571	14	BDU58594 Borna disease
4	564.6	98.9	1112	6	AR098533 Sequence
5	564.6	98.9	1112	6	AR108878 Sequence
6	564.6	98.9	8909	14	BD1311521 Borna dis
7	564.6	98.9	8910	6	AR098546 Sequence
8	564.6	98.9	8910	6	AR108891 Sequence
9	564.6	98.9	8910	14	BDU04608 Borna disease
10	563	98.6	571	6	AR432669 Sequence
11	563	98.6	571	14	BDU58596 Borna disease
12	561	98.2	8910	6	AR432655 Sequence
13	560.6	98.2	571	6	AR432667 Sequence
14	558.2	97.8	571	14	BDU58595 Borna disease
15	555	97.2	1110	14	BDU94867 Borna disease
16	553.4	96.9	8909	14	BD1311523 Borna dis
17	551.8	96.6	1110	14	BDU94863 Borna disease
18	551.8	96.6	3694	14	AY066023 Borna dis
19	540.6	94.7	1110	14	BDU94875 Borna disease

20	540.6	94.7	1110	14	BDU94879	U94879 Borna disease
21	540.6	94.7	1118	14	BDV38K	X68392 Borna Disease
22	540.6	94.7	1133	14	BDVPOLYMER	M99375 Borna disease
23	540.6	94.7	1851	14	S62821	S62821 p38-putative
24	540.6	94.7	8908	14	AY114161	AY114161 Borna dis
25	540.6	94.7	8908	14	AY114162	AY114162 Borna dis
26	540.6	94.7	8908	14	AY114163	AY114163 Borna dis
27	540.6	94.7	8908	14	BDV580	L27077 Borna disease
28	540.6	94.7	8909	14	BD1311522	AY11522 Borna dis
29	537.4	94.1	1113	14	AF158629	AF158629 Borna dis
30	531	92.0	1138	14	S67502S1	S67502 p40, p24 (B
31	529.4	92.7	1110	14	BDU94871	U94871 Borna disease
32	500.2	87.6	529	14	BD1246853	AJ246853 Borna dis
33	498.6	87.3	529	14	BD1246850	AJ246850 Borna dis
34	498.6	87.3	529	14	BD1246851	AJ246851 Borna dis
35	498.6	87.3	529	14	BD1246852	AJ246852 Borna dis
36	498.6	87.3	529	14	BD1246854	AJ246854 Borna dis
37	498.6	87.3	529	14	BD1246856	AJ246856 Borna dis
38	497	87.0	529	14	BD1246857	AJ246857 Borna dis
39	493.8	86.5	529	14	BD1246855	AJ246855 Borna dis
40	437.4	76.6	439	14	BDVPT1P40	X84691 Borna disease
41	434.2	76.0	439	14	BDAPF001613	AF001613 Borna dis
42	433.4	75.9	439	14	BD1250177	AJ250177 Borna dis
43	432.6	75.8	439	14	BDAPF001615	AF001615 Borna dis
44	431	75.5	439	14	BDAPF001610	AF001610 Borna dis
45	431	75.5	439	14	BDAPF001616	AF001616 Borna dis

ALIGNMENTS

RESULT 1	AR432668	571 bp	mRNA	linear	PAT 18-DEC-2003
LOCUS	Sequence 14 from patent US 6653464.				
DEFINITION	AR432668				
ACCESSION	AR432668.1	GI:40195247			
VERSION	AR432668.1	GI:40195247			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 571)				
AUTHORS	de la Torre, V.C.				
TITLE	Methods and compositions for screening for human Borna disease virus				
JOURNAL	Patent: US 6653464-A 14 25-NOV-2003;				
FEATURES	location/Qualifiers				
source	1..571				
	/organism="unknown"				
	/mol_type="mRNA"				
ORIGIN					
Query Match	100.0%; Score 571; DB 6; Length 571;				
Best Local Similarity	100.0%; Pred. No. 6e-171;				
Matches 571; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	TTCATACAGTAAAGCCGACCCGCTGTGTTCTATGTTCTATCCAGACTGACGCTG	60		
DB	1	TTCATACAGTAAAGCCGACCCGCTGTGTTCTATGTTCTATCCAGACTGACGCTG	60		
QY	61	CGTTTGTTCACGAGGGGTGCTGTAATCTTACCTTGACGCGCTGTGAG	120		
DB	61	CGTTTGTTCACGAGGGGTGCTGTAATCTTACCTTGACGCGCTGTGAG	120		
QY	121	AACGAGCTGTTTAAGCTCGAAGTTTACGGGGAAAGACGACGAGCTGATCTCA	180		
DB	121	AACGAGCTGTTTAAGCTCGAAGTTTACGGGGAAAGACGACGAGCTGATCTCA	180		
QY	181	CCGAGCTGAGATCTCTCTATCTTACGACCATTTGTTGCTCTATTAAGAGGTTGTA	240		
DB	181	CCGAGCTGAGATCTCTCTATCTTACGACCATTTGTTGCTCTATTAAGAGGTTGTA	240		
QY	241	TGAGTCTGCTCTTAAGTCAAGACGAGCCGACAGATCAAGAAAGTTTAAACTA	300		
DB	241	TGAGTCTGCTCTTAAGTCAAGACGAGCCGACAGATCAAGAAAGTTTAAACTA	300		

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.333 Seconds

(without alignment)
8003.565 Million cell updates/sec

Title: US-10-627-141-14

Sequence: 1 TTTCATACACTACAGCCGAC.....CTTACATCCCTGATGTC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: geneeqn19808:*
- 3: geneeqn20008:*
- 4: geneeqn2001as:*
- 5: geneeqn2001as:*
- 6: geneeqn2002as:*
- 7: geneeqn2002as:*
- 8: geneeqn2003as:*
- 9: geneeqn2003as:*
- 10: geneeqn2003as:*
- 11: geneeqn2003as:*
- 12: geneeqn2004as:*
- 13: geneeqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	567.8	99.4	571	2	AAV32853 Human Bor
3	564.6	98.9	8910	2	AAV38104 Borna dis
4	563	98.6	571	2	AAV32852 Human Bor
5	537.4	94.1	1113	4	AAAF61225 Borna dis
6	448	78.5	559	4	AAAF61230 Borna dis
7	90.4	15.8	501	6	AB136599 Human col
8	90.4	15.8	1047	4	AAH13875 Human col
9	90.4	15.8	1293	4	AAH161251 Human col
10	90.4	15.8	1293	10	AAH04080 Human col
11	90	15.8	721	4	AAH04080 Human col
12	88.8	15.6	1311	10	AAH07119 Human col
13	85.8	15.0	1626	12	AAH07119 Human col
14	83.8	14.7	1626	12	AAH07119 Human col
15	83.8	14.7	1626	12	AAH07119 Human col
16	83.8	14.7	1626	12	AAH07119 Human col
17	83.8	14.7	1626	12	AAH07119 Human col
18	76.4	13.4	1665	12	AAH07119 Human col
19	76.2	13.3	4940	10	AAH07119 Human col
20	76.2	13.3	4940	10	AAH07119 Human col

21	67.8	11.9	804	3	AACT7204 Human ORF
22	63.8	11.2	2843	4	AAH16588 Human CDN
23	60.6	10.6	712	6	ABT10107 Human bre
24	58.6	10.3	430	10	ADP80751 Human bre
25	57.2	10.0	1557	12	ADJ84332 Human phe
26	56.6	9.9	466	12	ADP66154 Human CDN
27	56	9.8	767	4	AAI96380 Human neu
28	44.6	7.8	836	4	AAI96519 Human neu
29	39.8	7.0	2000	8	ADA71938 Human neu
30	34.4	6.0	672	10	ADB55214 Human neu
31	34.4	6.0	672	10	ADB55214 Human neu
32	33.8	5.9	250	3	AACT7230 Human sec
33	33.8	5.9	553	4	AAH13122 Human sec
34	33.8	5.9	693	3	AAH75126 Human sec
35	33.6	5.9	588	4	AAH09596 Human CDN
36	32.8	5.7	4983	12	ADQ63005 Human CDN
37	32.4	5.7	4062	8	ADA71340 Human CDN
38	32.4	5.7	5642	4	AAK69744 Human imm
39	32.4	5.7	5642	5	AAK69744 Human imm
40	32.2	5.6	3515	2	AAK34694 Human DNA
41	32.2	5.6	110000	6	AAK20252 Borrelia
42	32.2	5.6	110000	6	AAK20252 Borrelia
43	32	5.6	709	4	AAQ67195_1 Human
44	32	5.6	711	4	AAK85690 Human imm
45	31.8	5.6	310	6	AB170681 Corn tass

ALIGNMENTS

RESULT 1
AAV32851 standard; CDNA; 571 BP.

AAV32851;

27-AUG-2003 (revised)
09-NOV-1998 (first entry)

Human Borna disease virus p40 CDNA.

BDV; infection; diagnosis; neuropsychiatric disorder; human; ss.

Borna disease virus.

Key Location/Qualifiers
CDS 3..569

FT /*tag= a

XX MO9830238-A1.

XX 16-JUL-1998.

XX 07-JAN-1998; 98MO-US000495.

XX 07-JAN-1997; 97US-00779764.

XX (SCRI) SCRIpps RES INST.

XX De la Torre JC;

XX WPI; 1998-398802/34.

XX P-PSDB; AAM49051.

XX New isolated human Borna disease nucleic acid(s) - which encode p24, p16,

XX p56, p40 and L polymerase catalytic domain poly:peptide(s), used to

XX develop products for detection.

XX Claim 13; Page 128; 207pp; English.

XX This CDNA sequence codes for p40 polypeptide (see AAM49051) of a Borna

XX disease virus (BDV) isolate (H1) obtained from a psychiatric patient with

XX a mood disorder. It can be produced by PCR (see also AAV32866-69) of CDNA

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:41:19 ; Search time 130.667 Seconds
(without alignments)
7150.362 Million cell updates/sec

Title: US-10-627-141-14

Perfect score: 571

Sequence: 1 TTCATACAGTAAGCCGACG.....CTTACATCCCTGTGTTGTC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	100.0	571	3	US-08-779-764A-14
2	571	100.0	571	4	US-09-563-456-14
3	567.8	99.4	571	3	US-08-779-764A-16
4	567.8	99.4	571	4	US-09-563-456-16
5	564.6	98.9	1112	3	US-08-369-822C-1
6	564.6	98.9	1112	3	US-08-582-776C-1
7	564.6	98.9	1112	3	US-08-434-831B-1
8	564.6	98.9	8910	3	US-08-369-822C-19
9	564.6	98.9	8910	3	US-08-582-776C-19
10	564.6	98.9	8910	3	US-08-434-831B-19
11	563	98.6	571	3	US-08-779-764A-15
12	563	98.6	571	4	US-09-563-456-15
13	561	98.2	8910	3	US-08-779-764A-1
14	561	98.2	8910	3	US-09-563-456-1
15	560.6	98.2	571	3	US-08-779-764A-13
16	560.6	98.2	571	4	US-09-563-456-13
17	33.8	5.9	250	4	US-09-513-999C-31305
18	32.4	5.7	29935	4	US-09-949-016-11871
19	32.4	5.7	29936	4	US-09-949-016-11871
20	31.6	5.5	36156	4	US-09-949-016-52358
21	31.6	5.5	36156	4	US-09-949-016-12128
22	31.6	5.5	36156	4	US-09-949-016-13261
23	31.4	5.5	398	4	US-09-621-876-8976
24	31.2	5.5	285	4	US-09-313-294A-3339
25	31.2	5.5	285	4	US-09-313-294A-6731
26	31.2	5.5	601	4	US-09-949-016-52357
27	31.2	5.5	601	4	US-09-949-016-52359

28	30.6	5.4	1524	4	US-09-270-767-13500	Sequence 13500, A
29	30.6	5.4	106929	4	US-09-949-016-12060	Sequence 12060, A
30	30.6	5.4	106929	4	US-09-949-016-16618	Sequence 16618, A
31	30.4	5.3	4352	4	US-09-620-312D-955	Sequence 555, App
32	30.2	5.3	46347	4	US-09-949-016-12469	Sequence 13469, A
33	30	5.3	601	4	US-09-949-016-130134	Sequence 130134, A
34	30	5.3	993	4	US-09-949-016-13516	Sequence 13516, A
35	30	5.3	21125	4	US-09-949-016-15108	Sequence 15108, A
36	30	5.3	23368	4	US-09-949-016-15418	Sequence 15418, A
37	30	5.3	25733	4	US-09-902-540-1215	Sequence 1215, App
38	30	5.3	260247	4	US-09-313-294A-4410	Sequence 4410, App
39	29.8	5.2	297	4	US-09-134-000C-3175	Sequence 3175, App
40	29.8	5.2	417	4	US-09-134-000C-3175	Sequence 3175, App
41	29.8	5.2	417	4	US-09-134-000C-3175	Sequence 3175, App
42	29.8	5.2	492	4	US-09-248-796A-13868	Sequence 13868, A
43	29.8	5.2	3789	4	US-09-107-433-2464	Sequence 2464, App
44	29.4	5.1	4175	1	US-07-934-333B-1	Sequence 1, Appl1
45	29.4	5.1	4175	1	US-08-278-089A-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-08-779-764A-14
; Sequence 14, Application US/08779764A
; Patent No. 6057094
; GENERAL INFORMATION:
; APPLICANT: de la Torre, Juan C.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
; TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
; STREET: 10550 No. 6057094th Torrey Pine Road, TPC-8
; CITY: La Jolla
; STATE: California
; COUNTRY: United States
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,764A
; FILING DATE: 16-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Filting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSRI 465.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 784-9399
; TELEFAX: (619) 784-2937
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-779-764A-14

Query Match 100.0%; Score 571; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 5.2e-193;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TTCATACAGTAAGCCGACGCTGTGTTCTATGTTGCTAATCCAGACTGCAGCTG 60
1 TTCATACAGTAAGCCGACGCTGTGTTCTATGTTGCTAATCCAGACTGCAGCTG 60
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 17:28:54 ; Search time 463 Seconds

(without alignments)
7464.304 Million cell updates/sec

Title: US-10-627-141-14

Perfect score: 571

Sequence: 1 TTCTACAGACGACCCACG.....CTTACAAATCCCTGATTGC 571

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 306245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	100.0	571	18	US-10-627-141-14
2	567.8	99.4	571	18	US-10-627-141-14
3	563	98.6	571	18	US-10-627-141-15
4	561	98.2	8910	18	US-10-627-141-15
5	560.6	98.2	571	18	US-10-627-141-13
6	90.4	15.8	488	9	US-09-878-178-188
7	90.4	15.8	488	13	US-10-046-935-188
8	90.4	15.8	488	14	US-10-146-502-188
9	88.8	15.6	1293	18	US-10-128-558-288
10	88.8	15.6	1311	18	US-10-128-558-61
11	76.4	13.4	1665	16	US-10-252-157-212

Result No.	Score	Query Match	Length	ID	Description
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13	58.4	10.2	1557	17	US-10-027-632-260709
14	57.2	10.0	1557	13	US-10-027-632-260703
15	57.2	10.0	1557	13	US-10-027-632-260704
16	57.2	10.0	1557	13	US-10-027-632-260705
17	57.2	10.0	1557	13	US-10-027-632-260706
18	57.2	10.0	1557	13	US-10-027-632-260707
19	57.2	10.0	1557	13	US-10-027-632-260708
20	57.2	10.0	1557	17	US-10-027-632-260708
21	57.2	10.0	1557	17	US-10-027-632-260704
22	57.2	10.0	1557	17	US-10-027-632-260705
23	57.2	10.0	1557	17	US-10-027-632-260706
24	57.2	10.0	1557	17	US-10-027-632-260707
25	57.2	10.0	1557	17	US-10-027-632-260708
26	56.6	9.9	466	18	US-10-637-855-146
27	56.6	9.9	305	17	US-10-242-535A-48642
28	33.4	5.8	305	17	US-10-085-783A-48642
29	33.2	5.8	347	18	US-10-425-115-141947
30	33.2	5.8	478	13	US-10-027-632-75475
31	33.2	5.8	478	13	US-10-027-632-75475
32	33.2	5.8	478	17	US-10-027-632-75475
33	33.2	5.8	478	17	US-10-027-632-109080
34	32.8	5.7	252	18	US-10-425-115-19793
35	32.8	5.7	674	18	US-10-425-115-19793
36	32.8	5.7	4483	19	US-10-437-963-8503
37	32.4	5.7	121410	18	US-10-741-600-17733
38	32.2	5.6	495269	17	US-10-398-221-8
39	32.2	5.6	3011208	17	US-10-398-221-2058
40	31.8	5.6	157	17	US-10-424-599-128364
41	31.8	5.6	310	9	US-09-294-0938-55
42	31.8	5.6	1456	13	US-10-027-632-76199
43	31.8	5.6	1456	17	US-10-027-632-76199
44	31.8	5.6	1748	18	US-10-425-115-112215
45	31.8	5.6	2124	18	US-10-425-115-6979

ALIGNMENTS

RESULT 1

US-10-627-141-14

Sequence 14, Application US/10627141

Publication No. US20040162421A1

GENERAL INFORMATION:

APPLICANT: de la Torre, Juan C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESS: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10550 North Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: California

COUNTRY: United States

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/627,141

FILING DATE: 25-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/779,764

FILING DATE: 16-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Filting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 465.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 13:08:09 ; Search time 2654 Seconds

(without alignments)
8189.411 Million cell updates/sec

Title: US-10-627-141-14

Sequence: 1 TTCAATACAGTAAAGCCGAC.....CTTAACATCCCTGATGTC 571

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:
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2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gest1:
9: gb_gest2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90.4	15.8	582	2	AM593371 hg13h11.x
2	90.4	15.8	1679	3	BC051316 Homo sapi
3	90	15.8	721	1	AU119718 AU119718
4	87.4	15.3	580	1	AI808337 w54f08.x
5	85.8	15.0	408	1	AA812109 cb40c08.x
6	77.8	13.6	661	6	CD705171 ES121698
7	76.4	13.4	685	5	BQ006526 UI-H-EU0
8	76.4	13.4	1790	3	BC033624 Homo sapi
9	76.4	13.4	1826	4	BC032471 Homo sapi
10	76.2	13.3	389	4	BM698664 UI-E-DX1
11	76.2	13.3	500	1	AL599858 DKFZP133C
12	76.2	13.3	725	5	BO183041 UT-H-EU0
13	76.2	13.3	932	6	CB993540 AGENCOURT
14	75.4	13.2	932	5	BM698664 UI-E-DX1
15	74.8	13.1	866	5	BX445843 BX445843
16	72.6	12.7	774	8	BZ135297 CB431776
17	71.4	12.5	548	1	AA001666 2h55c09.r
18	69.6	12.2	511	2	BR995306 IL0-MTC21
19	65.8	11.5	964	8	AG227224 HS_2017.B
20	64.2	11.2	455	8	AG227224 HS_2017.B
21	64	11.2	443	7	CF137776 UI-HF-BNO
22	63.8	11.2	470	5	BQ286427 IK30a01.Y
23	63.8	11.2	479	6	CB123801 K-EST0172
24	63.8	11.2	480	6	CB158377 K-EST0217

25	63.8	11.2	481	5	BQ271452 IK14B03.Y
26	63.8	11.2	595	5	CA948940 IG30C11.Y
27	63.8	11.2	641	5	BU951096 BU951096
28	63.8	11.2	733	6	CA707788 UI-H-FT1
29	63.8	11.2	750	6	CA757171 1097410.X
30	63.8	11.2	752	6	CA775929 CA775929
31	63.8	11.2	778	6	CA776003 1097410.X
32	63.8	11.2	781	6	CA778017 1P16H02.X
33	63.8	11.2	798	6	CA778017 1P16H02.X
34	63.8	11.2	1042	4	BM474332 AGENCOURT
35	63.4	11.1	437	8	BS4247 C17-HSP-201
36	62.8	11.0	454	7	CN360600 170006001
37	62.2	10.9	711	6	CA778310 CA778310
38	61.6	10.8	562	5	BQ271156 BQ271156
39	61.6	10.8	593	5	BU076047 BU076047
40	61.6	10.8	601	5	BQ269772 BQ269772
41	61.6	10.8	615	5	BU952536 BU952536
42	61.6	10.8	709	6	CD237377 FNPAD02
43	60.6	10.6	712	1	AA875998 ob93b09.s
44	60.2	10.5	558	7	CK005159 AGENCOURT
45	58.8	10.3	438	1	AI830973 WJ80F03.X

ALIGNMENTS

RESULT 1
LOCUS AM593371/c
DEFINITION hg13h11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2945541 3' similar to SW:VP40_BDV Q01552 40 KD PROTEIN. [2]
SW:VP40_BDV ; mRNA sequence.
AM593371
AM593371.1 GI:7280629

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gbpco
High quality sequence atdb: 464.
Location/Qualifiers

FEATURES

SOURCE

1. 582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2945541"
/lab host="DH10B"
/clone.lib="soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pRTT3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCB1) were mixed and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Benito
Soares and M. Fatima Bernaldo.

ORIGIN

Query Match

15.8%; Score 90.4; DB 2; Length 582;

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:35:04 ; Search time 2798 Seconds

(without alignment)
9888.466 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571
Sequence: 1 TTCAATACAGTAAAGCCGACCCAGC.....CTTACATCCCTGTAGTTGC 571

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:
1: gb_ba:*
2: gb_hg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sgs:*
12: gb_ey:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	6 AR432669	AR432669 Sequence
2	566.2	99.2	571	6 AR432670	AR432670 Sequence
3	566.2	99.2	571	14 BDUS8595	BDUS8595 Borna disease
4	563	98.6	571	6 AR432668	AR432668 Sequence
5	561.4	98.3	571	14 BDUS8596	BDUS8596 Borna disease
6	560.6	98.2	571	6 AR432667	AR432667 Sequence
7	559.8	98.0	1112	6 AR098533	AR098533 Sequence
8	559.8	98.0	1112	6 AR108878	AR108878 Sequence
9	559.8	98.0	8909	14 BD1311521	BD1311521 Borna disease
10	559.8	98.0	8910	6 AR098546	AR098546 Sequence
11	559.8	98.0	8910	6 AR108891	AR108891 Sequence
12	559.8	98.0	8910	14 BDUS8594	BDUS8594 Borna disease
13	558.2	97.8	571	14 BDUS8594	BDUS8594 Borna disease
14	556.2	97.4	8910	6 AR432655	AR432655 Sequence
15	550.2	96.4	1110	14 BDUS8594	BDUS8594 Borna disease
16	548.6	96.1	8909	14 BD1311523	BD1311523 Borna disease
17	547	95.8	1110	14 BDUS8594	BDUS8594 Borna disease
18	547	95.8	3694	14 AY066023	AY066023 Borna disease
19	535.8	93.8	1110	14 BDUS8594	BDUS8594 Borna disease

20	535.8	93.8	1110	14 BDUS8594	BDUS8594 Borna disease
21	535.8	93.8	1118	14 BDV38K	BDV38K Borna disease
22	535.8	93.8	1133	14 BDV38K	BDV38K Borna disease
23	535.8	93.8	1851	14 BDV38K	BDV38K Borna disease
24	535.8	93.8	8908	14 AY114161	AY114161 Borna disease
25	535.8	93.8	8908	14 AY114162	AY114162 Borna disease
26	535.8	93.8	8908	14 AY114163	AY114163 Borna disease
27	535.8	93.8	8908	14 BDV38K	BDV38K Borna disease
28	535.8	93.8	8908	14 BDV38K	BDV38K Borna disease
29	532.6	93.3	1113	14 AR158629	AR158629 Borna disease
30	526.2	92.2	1138	14 BDV38K	BDV38K Borna disease
31	524.6	91.9	1110	14 BDUS8594	BDUS8594 Borna disease
32	495.4	86.8	529	14 BD1246853	BD1246853 Borna disease
33	493.8	86.5	529	14 BD1246853	BD1246853 Borna disease
34	493.8	86.5	529	14 BD1246851	BD1246851 Borna disease
35	493.8	86.5	529	14 BD1246852	BD1246852 Borna disease
36	493.8	86.5	529	14 BD1246854	BD1246854 Borna disease
37	493.8	86.5	529	14 BD1246856	BD1246856 Borna disease
38	493.8	86.5	529	14 BD1246857	BD1246857 Borna disease
39	489	85.6	529	14 BD1246855	BD1246855 Borna disease
40	432.6	75.8	439	14 BDV38K	BDV38K Borna disease
41	429.4	75.2	439	14 BDV38K	BDV38K Borna disease
42	428.6	75.1	439	14 BD125017	BD125017 Borna disease
43	427.8	74.9	439	14 BDV38K	BDV38K Borna disease
44	426.2	74.6	439	14 BDV38K	BDV38K Borna disease
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ALIGNMENTS

RESULT 1	AR432669	571 bp	MRNA	linear	PAT 18-DEC-2003
LOCUS	AR432669	Sequence 15 from patent US 6653464.			
DEFINITION	AR432669				
ACCESSION	AR432669.1	GI:40195248			
VERSION					
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 571)				
TITLE	de la Torre, J.C.				
JOURNAL	Methods and compositions for screening for human Borna disease				
FEATURES	Patent: US 6653464-A 15 25-NOV-2003;				
ORIGIN	Location/Qualifiers				
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	/organism="unknown"				
	/mol_type="mrna"				

Query Match	100.0%	Score 571;	DB 6;	Length 571;
Best Local Similarity	100.0%	Pred. No. 6e-176;		
Matches 571;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	TTCAATACAGTAAAGCCGACCCAGCCTGTGTTTATAGTTGCTAATCCCGACGACCTG 60		
DB	1	TTCAATACAGTAAAGCCGACCCAGCCTGTGTTTATAGTTGCTAATCCCGACGACCTG 60		
OY	61	CGTTTGTTCACGAGGGGCTGCTGTAATCTACCTGAGCGCCATACAGCGGTGAG 120		
DB	61	CGTTTGTTCACGAGGGGCTGCTGTAATCTACCTGAGCGCCATACAGCGGTGAG 120		
OY	121	AACAGACTGTTGTTAAGACTGCGAGTTTACGGGGAAGAGACGACGATGATCTCA 180		
DB	121	AACAGACTGTTGTTAAGACTGCGAGTTTACGGGGAAGAGACGACGATGATCTCA 180		
OY	181	CCGAGCTGAGATCTCTCTATCTAGCATTTGCTCATTAATAGGGGTTGTGA 240		
DB	181	CCGAGCTGAGATCTCTCTATCTAGCATTTGCTCATTAATAGGGGTTGTGA 240		
OY	241	TAGATCTGCTGTTAAGATCAAGACGAGCCGACGATCAAGAAAGTTTAAAACTA 300		

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.333 Seconds
(without alignments)
8003.565 Million cell updates/sec

Title: US-10-627-141-15
Sequence: 1 TTCAATACGTAACGCCACG.....CTTACATCCTGTGATTGC 571

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
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- 8: Geneseq2003as:*
- 9: Geneseq2003bs:*
- 10: Geneseq2003cs:*
- 11: Geneseq2003ds:*
- 12: Geneseq2004as:*
- 13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	2	AAV32852 Human Bor
2	566.2	99.2	571	2	AAV32853 Human Bor
3	559.8	98.6	571	2	AAV32851 Human Bor
4	559.8	98.0	8910	2	AAV32851 Human Bor
5	532.6	93.3	1113	4	AAV32851 Human Bor
6	443.2	77.6	559	4	AAV32851 Human Bor
7	88.8	15.6	501	6	AAV32851 Human Bor
8	88.8	15.6	1047	4	AAV32851 Human Bor
9	88.8	15.6	1293	4	AAV32851 Human Bor
10	88.8	15.6	1293	4	AAV32851 Human Bor
11	88.8	15.6	1293	4	AAV32851 Human Bor
12	87.2	15.3	1311	10	AAV32851 Human Bor
13	87.2	15.3	1311	10	AAV32851 Human Bor
14	82.2	14.4	1626	12	AAV32851 Human Bor
15	82.2	14.4	1626	12	AAV32851 Human Bor
16	82.2	14.4	1626	12	AAV32851 Human Bor
17	82.2	14.4	1626	12	AAV32851 Human Bor
18	76.2	13.3	1665	10	AAV32851 Human Bor
19	76.2	13.3	1665	10	AAV32851 Human Bor
20	76.2	13.3	1665	10	AAV32851 Human Bor

21	66.2	11.6	804	3	AAV32852 Human Bor
22	63.8	11.2	2843	4	AAV32852 Human Bor
23	60	10.5	712	6	AAV32852 Human Bor
24	58.6	10.3	430	10	AAV32852 Human Bor
25	57.2	10.0	1557	12	AAV32852 Human Bor
26	56.6	9.9	466	12	AAV32852 Human Bor
27	56	9.8	767	4	AAV32852 Human Bor
28	45.8	8.0	836	4	AAV32852 Human Bor
29	37.6	6.6	672	10	AAV32852 Human Bor
30	37.6	6.6	672	10	AAV32852 Human Bor
31	37.4	6.5	2000	8	AAV32852 Human Bor
32	35.4	6.2	110000	6	AAV32852 Human Bor
33	35.4	6.2	110000	6	AAV32852 Human Bor
34	33.8	5.9	250	3	AAV32852 Human Bor
35	33.8	5.9	553	4	AAV32852 Human Bor
36	33.8	5.9	693	3	AAV32852 Human Bor
37	33.8	5.9	3515	2	AAV32852 Human Bor
38	33.6	5.9	588	4	AAV32852 Human Bor
39	33.2	5.8	349980	5	AAV32852 Human Bor
40	33.8	5.7	4983	12	AAV32852 Human Bor
41	33.6	5.7	181257	12	AAV32852 Human Bor
42	32.4	5.7	4062	8	AAV32852 Human Bor
43	32.4	5.7	5642	4	AAV32852 Human Bor
44	32.4	5.7	5642	5	AAV32852 Human Bor
45	32.2	5.6	883	2	AAV32852 Human Bor

ALIGNMENTS

RESULT 1
ID AAV32852 standard; CDNA; 571 BP.
XX AAV32852;
AC AAV32852;
XX 27-AUG-2003 (revised)
DT 09-NOV-1998 (first entry)
XX Human Borna disease virus p40 cDNA.
DE Human Borna disease virus p40 cDNA.
XX BDV; infection; diagnosis; neuropsychiatric disorder; human; ss.
XX OS Borna disease virus.
XX FH Key Location/Qualifiers
FT CDS 3..569 /*tag= a
XX PN WO9830238-A1.
XX PD 16-JUL-1998.
XX PF 07-JAN-1998; 98MO-US000495.
XX PR 07-JAN-1997; 97US-00779764.
XX PA (SCRI) SCRIPPS RES INST.
XX PI De La Torre JC;
XX DR WPI; 1998-398802/34.
XX DR P-PSDB; AAM49052.
XX PT New isolated human Borna disease nucleic acid(s) - which encode p24, p16,
XX PT p56, p40 and L polymerase catalytic domain polypeptide(s), used to
XX PT develop products for detection.
XX PS Claim 14; Page 128-129; 207pp; English.
XX CC This cDNA sequence codes for p40 polypeptide (see AAM49052) of a Borna
XX CC disease virus (BDV) isolate (H2) obtained from a psychiatric patient with
XX CC a mood disorder. It can be produced by PCR (see also AAV32866-69) of cDNA

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:41:19 ; Search time 130.667 Seconds

(without alignments)
7150.362 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571

Sequence: 1 TTCAATACAGTACGCCACG.....CTTACATCCCTGTAGTTGC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6C.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571	100.0	571	US-08-779-764A-15	Sequence 15, Appl
2	571	100.0	571	US-09-563-456-15	Sequence 15, Appl
3	566.2	99.2	571	US-08-779-764A-16	Sequence 16, Appl
4	566.2	99.2	571	US-09-563-456-16	Sequence 16, Appl
5	563	98.6	571	US-08-779-764A-14	Sequence 14, Appl
6	563	98.6	571	US-09-563-456-14	Sequence 14, Appl
7	560.6	98.2	571	US-08-779-764A-13	Sequence 13, Appl
8	560.6	98.2	571	US-09-563-456-13	Sequence 13, Appl
9	559.8	98.0	1112	US-08-369-822C-1	Sequence 1, Appl
10	559.8	98.0	1112	US-08-582-776C-1	Sequence 1, Appl
11	559.8	98.0	1112	US-08-434-831B-1	Sequence 1, Appl
12	559.8	98.0	8910	US-08-369-822C-19	Sequence 19, Appl
13	559.8	98.0	8910	US-08-582-776C-19	Sequence 19, Appl
14	559.8	98.0	8910	US-08-434-831B-19	Sequence 19, Appl
15	556.2	97.4	8910	US-08-779-764A-1	Sequence 1, Appl
16	556.2	97.4	8910	US-09-563-456-1	Sequence 1, Appl
17	34	6.0	29935	US-09-949-016-11871	Sequence 1, Appl
18	34	6.0	29936	US-09-949-016-14443	Sequence 1, Appl
19	33.8	5.9	250	US-09-513-999C-31305	Sequence 31305, A
20	33.8	5.9	399	US-09-621-976-8976	Sequence 8976, Ap
21	33.2	5.8	601	US-09-949-016-52358	Sequence 52358, A
22	33.2	5.8	36156	US-09-949-016-12128	Sequence 12128, A
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ALIGNMENTS

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US-08-779-764A-15
Sequence 15, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779, 764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-779-764A-15
Query Match 100.0%; Score 571; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 2.6e-196;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 TTCAATACAGTACGCCACCTTGTGTTCTATGTTGCTAATCCAGAGTCGACGCTG 60
1 TTCAATACAGTACGCCACCTTGTGTTCTATGTTGCTAATCCAGAGTCGACGCTG 60
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 17:28:54 / Search time 463 Seconds

(without alignments)
7464.304 Million cell updates/sec

Title: US-10-627-141-15

Perfect score: 571

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Post-processing:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	87.2	15.3	1311	US-10-128-558-61	Sequence 61, Appl
11	76.2	13.3	1665	US-10-252-157-212	Sequence 212, App

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ALIGNMENTS

RESULT 1

US-10-627-141-15

Sequence 15, Application US/10627141

Publication No. US2004016242A1

GENERAL INFORMATION:

APPLICANT: de la Torre, Juan C.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING OF HUMAN BORNA DISEASE VIRUS

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE

STREET: 10550 North Torrey Pines Road, TPC-8

CITY: La Jolla

STATE: California

COUNTRY: United States

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/627,141

FILING DATE: 25-Jul-2003

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/779,764

FILING DATE: 16-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSRI 465.0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 784-2937

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Title: US-10-627-141-15

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C 4	85.8	15.0	580	1	AI808337 v554f08.x
C 5	84.2	14.7	408	1	AA812109 CD705171
C 6	77.8	13.6	661	6	CD705171 EST21698
C 7	76.4	13.4	389	4	BQ006526 UI-H-E11-
C 8	76.2	13.3	389	4	BM698664 UI-E-DX1-
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C 13	76.2	13.3	1826	3	BC032471 Homo sapi
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C 21	65	11.4	437	8	BG110978 B54247
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C 33	63.8	11.2	781	6	CA778017 CA778017
C 34	63.8	11.2	798	6	CA776148 CA776148
C 35	63.8	11.2	1042	6	BM474332 BM474332
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C 38	61.6	10.8	562	5	BO271156 BO271156
C 39	61.6	10.8	593	5	BO276047 BO276047
C 40	61.6	10.8	601	5	BQ269772 BQ269772
C 41	61.6	10.8	615	5	BQ952536 BQ952536
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ALIGNMENTS

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IMAGE:2945541 3' similar to SW:VP40_BDV Q01552 40 KD PROTEIN. [2]
SW:VP40_BDV / mRNA sequence.

ACCESSION AM593371 GI:7280629
VERSION AM593371
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-tr@mail.nih.gov

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40up from Gibco
High quality sequence stop: 464.

FEATURES

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NCI CGAP GCBI) were mixed, and as circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

ORIGIN

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17	551.8	96.6	1110	14	BDU94875	BDU94875 Borna disease
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ALIGNMENTS

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AUTHORS	de la Torre,J.C.								
TITLE	Methods and compositions for screening for human Borna disease virus								
JOURNAL	Patent: US 6653464-A 16 25-NOV-2003;								
FEATURES	Location/Qualifiers								
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ORIGIN

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 11:37:54 ; Search time 422.313 Seconds
(without alignments)
8003.565 Million cell updates/sec

Title: US-10-627-141-16
Perfect score: 571

Sequence: 1 TTCATCAGTACAGCCGACG.....CTTACATCCCTGTAAGTGC 571

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 segs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: geneseqn2001as:*
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6: geneseqn2002as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	100.0	571	2	AAV32853
2	567.8	99.4	571	2	AAV32851
3	566.2	99.2	571	2	AAV32852
4	564.6	98.9	8910	2	AAV38104
5	537.4	94.1	1113	4	AAFe1225
6	448	78.5	559	4	AAFe1230
7	90.4	15.8	501	6	ABL36599
8	90.4	15.8	1047	4	AAH13875
9	90.4	15.8	1293	4	AAH1251
10	90.4	15.8	1293	10	ADBE0888
11	90	15.8	721	4	AAH04080
12	88.8	15.6	1311	10	ADBE07119
13	85.8	15.0	981	4	AAI59465
14	83.8	14.7	1626	12	ADDO0623
15	83.8	14.7	1626	12	ADDO0623
16	83.8	14.7	1626	12	ADDO0623
17	83.8	14.7	1626	12	ADDO0623
18	76.2	13.3	1665	10	ADDE53865
19	76.2	13.3	4940	10	ADFE82143
20	76.2	13.3	4940	10	ADFE82144

21	67.8	11.9	804	3	AACT7204
22	63.8	11.2	2843	4	AAH16588
23	60.6	10.6	712	6	ABT10107
24	58.6	10.3	430	10	ADBE0751
25	57.2	10.0	1557	12	ADH84332
26	56.6	9.9	466	12	ADPE6154
27	56	9.8	767	4	AAI96380
28	45.8	8.0	836	4	AAI96519
29	38.6	6.8	2000	8	ADA71938
30	36	6.3	672	10	ADBS5214
31	36	6.3	672	10	ADBA9727
32	35.4	6.2	693	3	AAAF5126
33	33.8	5.9	250	3	AACT7230
34	33.8	5.9	553	4	AAH13122
35	33.8	5.9	35515	2	AAK20252
36	33.6	5.9	588	4	AAH09586
37	33.2	5.8	34980	5	AAH86431
38	32.8	5.7	4983	12	ADQ63005
39	32.6	5.7	181257	12	ADFE69677
40	32.4	5.7	4062	8	ADA71340
41	32.4	5.7	5642	4	AAK69744
42	32.4	5.7	5642	5	AAK34694
43	32.2	5.6	883	2	AAK20351
44	32.2	5.6	110000	6	ABQ69245_16
45	32.2	5.6	110000	6	ABQ67195_1

ALIGNMENTS

RESULT 1	AAV32853	AAV32853 standard; cDNA; 571 BP.
ID	AAV32853	
XX	AAV32853	
AC	AAV32853	
DT	27-AUG-2003	(revised)
DT	09-NOV-1998	(first entry)
XX		
DE	Human Borna disease virus p40 cDNA.	
XX		
KW	BDV, infection; diagnosis; neuropsychiatric disorder; human; ss.	
XX		
OS	Borna disease virus.	
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FH	Key	Location/Qualifiers
FT	CDS	3..569
FT		/*tag= a
XX		
PN	WO9830238-A1.	
XX		
PD	16-JUL-1998.	
XX		
PF	07-JAN-1998;	98WO-US000495.
XX		
PR	07-JAN-1997;	97US-00779764.
XX		
PA	(SCRI) SCRIPPS RES INST.	
XX		
FI	De La Torre JC;	
XX		
DR	WPI; 1998-398802/34.	
XX		
DR	P-PSDB; AAM49053.	
XX		
PT	New isolated human Borna disease nucleic acid(s) - which encode p24, p16, p56, p40 and L polymerase catalytic domain poly:peptide(s), used to develop products for detection.	
PT	Claim 15; Page 129; 207pp; English.	
XX		
PS	This cDNA sequence codes for p40 polypeptide (see AAM49053) of a Borna disease virus (BDV) isolate (H3) obtained from a psychiatric patient with a mood disorder. It can be produced by PCR (see also AAV32866-69) of cDNA	
CC		
CC		

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 14:41:19 ; Search time 130.667 Seconds

(without alignments)
7150.362 Million cell updates/sec

Title: US-10-627-141-16

Perfect score: 571

Sequence: 1 TTATACAGTAAGCCGCCAGC.....CTTACATCCCTGTAGTTC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/prodata/1/ina/5A COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	571	100.0	571	US-09-563-456-16	Sequence 16, Appl
3	567.8	99.4	571	US-08-779-764A-14	Sequence 14, Appl
4	567.8	99.4	571	US-09-563-456-14	Sequence 14, Appl
5	566.2	99.2	571	US-08-779-764A-15	Sequence 15, Appl
6	566.2	99.2	571	US-09-563-456-15	Sequence 15, Appl
7	564.6	98.9	1112	US-08-369-822C-1	Sequence 1, Appl
8	564.6	98.9	1112	US-08-369-822C-1	Sequence 1, Appl
9	564.6	98.9	8910	US-08-434-831B-1	Sequence 1, Appl
10	564.6	98.9	8910	US-08-369-822C-19	Sequence 19, Appl
11	564.6	98.9	8910	US-08-582-776C-19	Sequence 19, Appl
12	564.6	98.9	8910	US-08-582-776C-19	Sequence 19, Appl
13	561	98.2	8910	US-08-434-831B-1	Sequence 1, Appl
14	561	98.2	8910	US-08-779-764A-1	Sequence 1, Appl
15	560.6	98.2	571	US-09-563-456-1	Sequence 1, Appl
16	560.6	98.2	571	US-08-779-764A-13	Sequence 13, Appl
17	34	6.0	29935	US-09-563-456-13	Sequence 13, Appl
18	34	6.0	29935	US-09-563-456-13	Sequence 13, Appl
19	33.8	5.9	250	US-09-949-016-11871	Sequence 11, Appl
20	33.2	5.8	601	US-09-513-999C-31305	Sequence 11, Appl
21	33.2	5.8	36156	US-09-949-016-14443	Sequence 14, Appl
22	33.2	5.8	36156	US-09-949-016-14443	Sequence 14, Appl
23	32.8	5.7	601	US-09-949-016-12128	Sequence 12, Appl
24	32.8	5.7	601	US-09-949-016-12128	Sequence 12, Appl
25	31.4	5.5	399	US-09-949-016-52357	Sequence 12, Appl
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27	31.2	5.5	291	US-09-313-294A-3339	Sequence 33, Appl

28	30.6	5.4	1524	US-09-270-767-13500	Sequence 13500, A
29	30.6	5.4	83617	US-09-949-016-12254	Sequence 12254, A
30	30.4	5.3	4352	US-09-620-312D-555	Sequence 555, App
31	30.2	5.3	46347	US-09-949-016-13469	Sequence 13469, A
32	30	5.3	930	US-09-248-796A-8265	Sequence 8265, App
33	30	5.3	4291	US-09-351-200-1	Sequence 1, Appl
34	30	5.3	25733	US-09-902-540-1215	Sequence 1215, App
35	30	5.3	260247	US-09-949-016-11358	Sequence 11358, App
36	29.8	5.2	417	US-09-313-294A-4410	Sequence 4410, App
37	29.8	5.2	417	US-09-134-000C-3173	Sequence 3173, App
38	29.8	5.2	417	US-09-134-000C-3175	Sequence 3275, App
39	29.8	5.2	492	US-09-248-796A-13868	Sequence 13868, App
40	29.6	5.2	3789	US-09-107-433-2464	Sequence 2464, App
41	29.6	5.2	1251	US-09-270-767-130447	Sequence 13044, App
42	29.6	5.2	1752	US-09-270-767-14305	Sequence 14305, App
43	29.6	5.2	33663	US-09-949-016-15679	Sequence 15679, A
44	29.4	5.1	59240	US-09-949-016-11933	Sequence 11933, A
45	29.4	5.1	63544	US-09-949-016-14025	Sequence 14025, A

ALIGNMENTS

```
RESULT 1
US-08-779-764A-16
Sequence 16, Application US/08779764A
Patent No. 6057094
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SCREENING
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESS: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 No. 6057094th Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764A
FILING DATE: 16-DEC-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-779-764A-16
Query Match 100.0%; Score 571; DB 3; Length 571;
Best Local Similarity 100.0%; Pred. No. 6, 2e-193;
Matches 571; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 17:28:54 ; Search time 463 Seconds
(without alignments)
7464.304 Million cell updates/sec

Title: US-10-627-141-16

Perfect score: 571

Sequence: 1 TTCACAGTAAGACCCACG.....CTTACATCCCTTACTTGC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 302624599 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	567.8	99.4	571	US-10-627-141-14	Sequence 14, Appl
3	566.2	99.2	571	US-10-627-141-15	Sequence 15, Appl
4	561	98.2	8910	US-10-627-141-1	Sequence 1, Appl
5	560.6	98.2	571	US-10-627-141-13	Sequence 13, Appl
6	90.4	15.8	498	US-09-878-178-188	Sequence 188, App
7	90.4	15.8	498	US-10-046-935-188	Sequence 188, App
8	90.4	15.8	498	US-10-146-502-188	Sequence 188, App
9	90.4	15.8	1293	US-10-128-558-288	Sequence 288, App
10	88.8	15.6	1311	US-10-128-558-61	Sequence 61, Appl
11	76.2	13.3	1665	US-10-252-157-212	Sequence 212, App

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C 14	57.2	10.0	1557	13	US-10-027-632-260703	Sequence 260703,
C 15	57.2	10.0	1557	13	US-10-027-632-260704	Sequence 260704,
C 16	57.2	10.0	1557	13	US-10-027-632-260705	Sequence 260705,
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C 18	57.2	10.0	1557	13	US-10-027-632-260707	Sequence 260707,
C 19	57.2	10.0	1557	13	US-10-027-632-260708	Sequence 260708,
C 20	57.2	10.0	1557	17	US-10-027-632-260703	Sequence 260703,
C 21	57.2	10.0	1557	17	US-10-027-632-260704	Sequence 260704,
C 22	57.2	10.0	1557	17	US-10-027-632-260705	Sequence 260705,
C 23	57.2	10.0	1557	17	US-10-027-632-260706	Sequence 260706,
C 24	57.2	10.0	1557	17	US-10-027-632-260707	Sequence 260707,
C 25	57.2	10.0	1557	17	US-10-027-632-260708	Sequence 260708,
C 26	56.6	9.9	466	18	US-10-637-855-146	Sequence 146, App
C 27	34	6.0	121410	19	US-10-741-600-17733	Sequence 17733, A
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C 29	33.4	5.8	305	17	US-10-085-783A-49642	Sequence 49642, A
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C 34	33.2	5.8	478	17	US-10-027-632-75475	Sequence 75475, A
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C 37	33.2	5.8	1233	13	US-10-027-632-251154	Sequence 251154,
C 38	33.2	5.8	1323	17	US-10-027-632-251152	Sequence 251152,
C 39	33.2	5.8	1323	17	US-10-027-632-251154	Sequence 251154,
C 40	32.8	5.7	252	18	US-10-425-115-19793	Sequence 19793, A
C 41	32.8	5.7	674	18	US-10-425-115-71387	Sequence 71387, A
C 42	32.8	5.7	1323	13	US-10-027-632-251151	Sequence 251151,
C 43	32.8	5.7	1323	13	US-10-027-632-251153	Sequence 251153,
C 44	32.8	5.7	1323	17	US-10-027-632-251151	Sequence 251151,
C 45	32.8	5.7	1323	17	US-10-027-632-251153	Sequence 251153,

ALIGNMENTS

RESULT 1
US-10-627-141-16
Sequence 16, Application US/10627141
Publication No. US20040162421A1
GENERAL INFORMATION:
APPLICANT: de la Torre, Juan C.
TITLE OF INVENTION: OF HUMAN BORNA DISEASE VIRUS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE SCRIPPS RESEARCH INSTITUTE
STREET: 10550 North Torrey Pines Road, TPC-8
CITY: La Jolla
STATE: California
COUNTRY: United States
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/627,141
FILING DATE: 25-Jul-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/779,764
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 465.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937

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OM nucleic - nucleic search, using sw model

Run on: April 4, 2005, 13:08:09 ; Search time 2654 Seconds

(without alignments)
8189,411 Million cell updates/sec

Title: US-10-627-141-16

Perfect score: 571
Sequence: 1 TTATACAGTACGACCCACG.....CTTACATCCTCTAGTTC 571

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
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9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 5	85.8	15.0	408	1	AA812109
C 6	77.8	13.6	661	6	CD705171 EST21698
C 7	76.4	13.4	685	5	BQ006517
C 8	76.2	13.3	389	4	BM698664 UI-H-E11-
C 9	76.2	13.3	500	1	AL599858 DKFZ313C
C 10	76.2	13.3	725	5	BQ183041 UI-H-E10-
C 11	76.2	13.3	737	6	CB993540
C 12	76.2	13.3	1790	3	BC033624
C 13	76.2	13.3	1826	3	BC032471 Homo sapi
C 14	75.2	13.2	932	5	BM445843 BX445843
C 15	74.6	13.1	866	5	BX431776 BX431776
C 16	72.6	12.7	774	8	BZ135297 CH230-287
C 17	71.4	12.5	548	1	AA001666
C 18	69.6	12.2	511	2	BF895306
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C 21	64	11.2	443	7	CF137776 UI-HF-BNO
C 22	63.8	11.2	479	6	BQ286427
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C 24	63.8	11.2	480	6	CB158377 K-EST0217

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29	63.8	11.2	750	6	CA775717
30	63.8	11.2	752	6	CA775929
31	63.8	11.2	778	6	CA776003
32	63.8	11.2	781	6	CA778017
33	63.8	11.2	798	6	CA778017
34	63.8	11.2	1042	4	BM474332
35	63.8	11.1	437	8	BM42427
36	62.4	11.0	454	7	CN360600
37	62.2	10.9	711	6	CA778310
38	61.6	10.8	562	5	BQ271156
39	61.6	10.8	593	5	BU076047
40	61.6	10.8	601	5	BQ269772
41	61.6	10.8	615	5	BU952536
42	61.6	10.8	709	6	CD237377
43	60.6	10.6	712	1	AA875998
44	60.2	10.5	558	7	CK005159
45	58.8	10.3	438	1	AI830973

ALIGNMENTS

RESULT 1
AM593371/c
LOCUS
DEFINITION
hg13h11.x1 Soares_NFL_T_GBC_S1 Homo sapiens CDNA clone
IMAGE:2945541 3' similar to SW:VP40_BDV Q01552 40 KD PROTEIN. [2]
SW:VP40_BDV /, mRNA sequence.

ACCESSION
AM593371
VERSION
AM593371.1 GI:7280629

SOURCE
EST.
Homo sapiens (human)

ORGANISM
Homo sapiens

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapb-remail.nih.gov

FEATURES
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40UP from Gibco

High quality sequence stop: 464.
Location/Qualifiers

1..582
Location/Qualifiers

1..582
Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

1..582
Location/Qualifiers

Query Match

15.8%, Score 90.4, DB 2, Length 582;

ORIGIN

1..582
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2945541"
/lab_host="DH10B"
/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: pTR73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell)
NCI CGAP (GCB) were mixed, and as circles were made in
vivo. Following HAP purification, this DNA was made in
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
1 M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bernaldo."